biochemical test. Genotypes of these strains were verified by PCR. Polymerase chain reaction was used to determine the following genes encoding colicins. The inhibitory activity of the CEC strains were evaluated against DEC K99 using an agar diffusion technique. Inhibitory activity was demonstrated by a clear zone around the spots.

Results: Approximately 100% of *E. coli* isolates were contained at least one gene of colicin. The prevalence of several classes of colicin was determined. As a result the most and the least detected genes were (Ia Ib, V, ANS4) and (M). Approximately 35% of all CEC strains produced inhibitory activity against DEC K99 ($P < 0.05$).

Conclusion: The growth of DEC K99 restricted by CEC strains producing colicin in vitro. The major area of opportunity for bacteriocin application into animal production is the control of foodborne pathogens.

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Evaluation of pathogen reduction systems to inactivate dengue and chikungunya viruses in apheresis platelets suspended in plasma

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Background: The potential risk of blood-borne transmission of infectious diseases has led to an increasing awareness to the need for a safe and effective pathogen reduction technology. This study evaluated the efficacy of two potential pathogen reduction systems to inactivate dengue virus (DENV) and chikungunya virus (CHIKV) in contaminated apheresis platelets (APLT) concentrates.

Methods: Double dose APLTs (n = 3) were split evenly and inoculated with 107 infectious units of DENV-2 or CHIKV. APLTs samples were assayed for infectivity before and after the Amotosalen photochemical treatment (PCT) or Riboflavin Pathogen Reduction treatment (PRT). Viral infectivity was determined by plaque assays and by observation of cell cytopathic effects (CPE) and immunofluorescent assay (IFA) of i*n vitro* cultures. The platelet (PLT) count, pH and residual S-59 were also determined over a period of five days.

Results: Amotosalen PCT showed robust efficacy of inactivation of viruses to reduction factors of greater than 4 log by plaque assays. Riboflavin PRT had varying degrees of DENV-2 and CHIKV reductions, ranging from 0.76 to 6.85 log. Residual, infective CHIKV that failed to be detected by plaque assay were however detected by CPE and IFA in cultures. This suggests that alternate assay methods are essential to support the evaluation of pathogen inactivation systems. The PLT count, pH, and residual S-59 of all treated APLTs were within the acceptable range for PLT viability and transfusion use although significant differences were detected between the pre- and post-treated APLTs over the storage period.

transmission via the transfusion of contaminated blood products.

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Molecular characterization of *Vibrio cholerae* isolated from the aquatic sources in Southern Kerala, India

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Background: Cholera, a life-threatening diarrhoeal disease is caused by the toxigenic strains of *Vibrio cholerae*. Very limited information is available on the molecular characteristics of environmental isolates of *V. cholerae* from Kerala, India, though this has been well studied in clinical strains. In the present study 29 environmental strains and one clinical strain were characterized for the presence of virulence-associated genes and novel variants of *tcpA* gene. Role of SXT and integrons in conferring drug resistance were also studied.

Methods: *V.cholerae* strains were isolated from different representative aquatic biotopes in Kerala, India. The species and serogroup identity was confirmed by specific PCR assay. Genomic DNA was extracted by Wizard Genomic DNA purification kit. Reverse trascriptase PCR was performed to determine the expression of *tcpA* genes. Phylogenetic tree & sequence analysis by BioEdit & MEGA programme. Antibiotic susceptibility by disc diffusion method and minimum inhibitory concentration by E- test. PCR assays for detection of drug resistant gene, SXT, integrons and virulence profile.

Results: The results indicated that only three were toxigenic - two from O56 and one from O1 serogroup. A multiplex PCR was developed for rapid identification of virulence associated genes. Six strains showed positive results for *tcpA* gene. Of these, two O1 strains showed El Tor specific *tcpA* gene. Other strains harboured variants of *tcpA* gene and showed considerable sequence polymorphism. The expression of *tcpA* gene showed a clear expression of all variant alleles in toxin co-regulated pilus (TCP) inducing conditions. Antibiogram analysis suggested that all strains except two were multi-drug resistant. MIC value for tetracycline and ciprofloxacin in O1 strains were relatively higher than that of non-O1/non-O139 strains.

Conclusion: Strains of O56 serogroup possessed variants of *tcpA* gene with large number of polymorphic sites at C-terminal end of the predicted protein sequence. The expression of variant alleles of *tcpA* gene was demonstrated. Majority of isolates showed multi-drug resistance phenotype. A few strains exhibited resistance to drugs commonly administered for treatment of diarrhoe. The O1 El Tor strains showed high level of resistance to ciprofloxacin and tetracycline compared to non-O1/non-O139 strains. The SXT element and integrons contribute to multi-drug resistance.

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